



SEQUENCE LISTING

<110> Piechaczyk, Marc
Noel, Daniele

<120> Biological material for treating a mammal by antibody gene transfer and pharmaceutical composition containing same

<130> 19904-002

<140> US 09-341,894

<141> 1998-01-16

<150> FR97/00540

<151> 1997-01-20

<160> 4

<170> PatentIn version 3.1

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<211> 420

<212> DNA

<213> Mus musculus

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<221> CDS<222> (1)..(420)

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<221> misc_feature<222> (1)..(420)

<223> Sequence coding for the variable region of the antibody heavy chain

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<221> sig_peptide<222> (1)..(57)

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Met Gly Trp Leu Trp Asn Leu Leu Phe Leu Met Ala Ala Ala Gln Ser

1 5 10 15

gcc caa gga cag atc cac ttg gta cag tct gga cct gag ctg aag aag 96

Ala Gln Gly Gln Ile His Leu Val Gln Ser Gly Pro Glu Leu Lys Lys

20 25 30

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 144

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

aca tcg tat ggc ttg acc tgg gtg ata cag tct cca gga aag gat tta 192

Thr Ser Tyr Gly Leu Thr Trp Val Ile Gln Ser Pro Gly Lys Asp Leu

50 55 60

aaa tgg atg ggc tgg ata aac acc ttc tct gga gtg cca aca tat gct 240

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Lys Trp Met Gly Trp Ile Asn Thr Phe Ser Gly Val Pro Thr Tyr Ala
 65 70 75 80
 gat gac ttc aag gga cgc ttt gcc ttc tct ttg gac acc tct acc agc 288
 Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Thr Ser
 85 90 95
 act gcc tat ttg cag atc gac aac ctc aaa aat gag gac acg gct aca 336
 Thr Ala Tyr Leu Gln Ile Asp Asn Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110
 tat ttc tgt tca aga agg ggg ggt ttt att act acg gct ctt gac acc 384
 Tyr Phe Cys Ser Arg Arg Gly Gly Phe Ile Thr Thr Ala Leu Asp Thr
 115 120 125
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 Trp Gly Gln Gly Thr Ser Leu Thr Val Ser Ser Ala
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Met Gly Trp Leu Trp Asn Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
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Ala Gln Gly Gln Ile His Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Ser Tyr Gly Leu Thr Trp Val Ile Gln Ser Pro Gly Lys Asp Leu
 50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Phe Ser Gly Val Pro Thr Tyr Ala
 65 70 75 80

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Thr Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Asp Asn Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Ser Arg Arg Gly Gly Phe Ile Thr Thr Ala Leu Asp Thr
 115 120 125

Trp Gly Gln Gly Thr Ser Leu Thr Val Ser Ser Ala
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tcc aat agt aat gtt gtg atg acc caa act cca ctc tcc ctg tct gtc 96
 Ser Asn Ser Asn Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val
 20 25 30

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc att 144
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
 35 40 45

gta cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca 192
 Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
 50 55 60

ggc cag tct cca aag ctc ctg atc tat aaa gtt tcc aac cga ttg tct 240
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Leu Ser
 65 70 75 80

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gac ttc aca 288
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

ctc aaa atc agc aga gtg gag gct gag gat ctg gga ctt tat tac tgt 336
 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
 100 105 110

ttt caa ggt tca cat att cca ttc acg ttc ggt tgc ggg aca aag ttc 384
Phe Gln Gly Ser His Ile Pro Phe Thr Phe Gly Ser Gly Thr Lys Phe
115 120 125

gaa ata aaa cgg gct gat gct gca cca act gta tcc 420
Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser
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Met Lys Leu Pro Gly Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Asn Ser Asn Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val
20 25 30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
35 40 45

Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Leu Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
100 105 110

Phe Gln Gly Ser His Ile Pro Phe Thr Phe Gly Ser Gly Thr Lys Phe
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser
130 135 140